THE PHYLOGENETIC POSITION OF THE SPONGE SPONGOSORITES SUBERITOIDES DETERMINED BY ANALYSIS OF 28S RRNA GENE SEQUENCE. Memoirs of the Oueensland Museum 44: 352. 1999:- A number of problems exist in the phylogenetic consideration of the sponge Spongosorites suberitoides that cannot be resolved on morphological grounds alone. Placing the sponge in the genus Spongosorites divides this genus into two groups; a single shallow water species and many deep-water species. Described differences between these groups include; oxea size, aerophobic colour-change and surface texture. Further, S. suberitoides shows an affinity with hadromerid sponges such as colour in life, texture, arrangement of anastomosing choanosomal tracts and the lack of an aerophobic reaction. In its association with hermit crabs and gastropods it resembles the genus Suberites.

It also shows similarities to species of *Aaptos* and some Polymastiidae. The DNA sequence of the five prime region of the 28S ribosomal gene of *S. suberitoides* is compared with DNA sequences from hadromerid and halichondrid species in a phylogenetic analysis to resolve the position of this species. *D Porifera, phylogeny, morphology, DNA, 28S ribosomal gene.* 

Grace P. McCormack (email: ginccormack(@ nhm.ac.uk), James O. McInerney & Michelle Kelly\*, Department of Zoology, The Natural History Museum, Cronwell Rd, London, SW7 5BD, UK: Floyd R. Sanford, Biology Department, Coe College, 1220 First Ave, NE, Cedar Rapids, Jowa 52402-5092, USA, \* Present address: Marine Ecology and Aquaculture, National Institute of Water & Atmospheric Research (NIWA), Private Bag 109-695, Newmarket, Anckland, New Zealand: 1 June 1998.

**PHYLOGENY OF LITHISTID SPONGES.** *Memoirs of the Queensland Museum 44: 352, 1999;*-Kelly-Borges and Pomponi (1994) utilised partial 18S rRNA gene sequences to resolve relationships within lithistid sponges (Porifera: Demospongiac). While their results lent weight to the growing realisation that the Order Lithistida is polyphyletic, their conclusions were hampered by low levels of sequence variation. Our initial study sought to evaluate the resolution potential between regions of the 18S and 28S rRNA genes within a group of selected Porifera. Approximately 1,300bp of the 18S rRNA gene and a 5' region of the 28S rRNA gene were compared with the data of Kelly-Borges and Pomponi (1994). Six taxa were selected which represented a gradient of relationships, ranging through the taxonomic levels of

genus, family and class. We found that the 700bp of the 28S rRNA gene presented the greatest potential for resolution of this group of porifera at the genus and family level, and that this molecular phylogeny is congruent with morphological hypotheses for the group. The study has progressed to include a number of other lithistid and non-lithistid taxa.  $\Box$  *Porifera, Lithistida, 18S rRNA, 28S rRNA, phylogeny.* 

James O. McIneruey (email: j.mcinerney(@nhm.ac.uk) & Michelle Kelly\*, Department of Zoology; The Natural History Museum, Cronwell Road, London SW7 5BD, UK; \* Present address: Marine Ecology and Aquaculture, National Institute of Water & Atmospheric Research (NIWA), Private Bag 109-695, Newmarket, Anekland, New Zealand; 1 June 1998